



SEQUENCE LISTING

<110> Tian, Hui
Zhao, Jiagang
Chen, Jin-Long
Cutler, Gene
An, Songzhu
Dai, Kang
Gupte, Jamila S.
Tularik Inc.

<120> Novel Receptors

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<141> 2001-11-21

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<151> 2000-11-22

<150> US 60/257,636

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<151> 2001-03-28

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<170> PatentIn Ver. 2.1

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melanin-concentrating hormone receptor 2 (MCHr2)

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Lys Thr Val Pro Asp Ile Tyr Ile Cys Asn Leu Ala Val Ala Asp Leu
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Val His Ile Val Gly Met Pro Phe Leu Ile His Gln Trp Ala Arg Gly
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Gly Glu Trp Val Phe Gly Gly Pro Leu Cys Thr Ile Ile Thr Ser Leu
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Phe Lys Asp Gly Val Glu Ser Cys Ala Phe Asp Leu Thr Ser Pro Asp
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Asp Val Leu Trp Tyr Thr Leu Tyr Leu Thr Ile Thr Thr Phe Phe Phe
195          200          205
Pro Leu Pro Leu Ile Leu Val Cys Tyr Ile Leu Ile Leu Cys Tyr Thr
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245          250          255
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<213> Homo sapiens

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<223> human G-protein coupled receptor (GPCR) TGR339

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35 40 45
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50 55 60
Tyr Phe Val Asn Met Ala Val Ala Gly Leu Val Leu Ser Ala Leu Ala
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Val Gly Gly Glu Val His Val Ala Leu Gln Ile Pro Phe Asn Val Ser
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115 120 125
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<223> human G-protein coupled receptor (GPCR) TGR346

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 35 40 45
 Val Leu Thr Gly Val Leu Ile Phe Ala Leu Ala Leu Phe Gly Asn Ala
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 Leu Val Phe Tyr Val Val Thr Arg Ser Lys Ala Met Arg Thr Val Thr
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 Asn Ile Phe Ile Cys Ser Leu Ala Leu Ser Asp Leu Leu Ile Thr Phe
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 Gly Ser Pro Met Trp His Val Gln Gln Leu Glu Ile Lys Tyr Asp Phe
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 Leu Tyr Glu Lys Glu His Ile Cys Cys Leu Glu Glu Trp Thr Ser Pro
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 Glu Asn Phe Lys Lys Asn Val Leu Ser Ala Val Cys Tyr Cys Ile Val
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 35 40 45
 Lys Thr Glu Gln Leu Ile Thr Leu Trp Val Leu Phe Val Phe Thr Ile
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 Val Gly Asn Ser Val Val Phe Ser Thr Trp Arg Arg Lys Lys Lys
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 Ser Arg Met Thr Phe Phe Val Thr Gln Leu Ala Ile Thr Asp Ser Phe
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tctttgttta aaagtgtgtg gtacctccca cctctctctc ttgctcctgc tctggccatg 1500
taagacgtgc ctgcttcccc ttcaccttct tgcattgatt taagtttctt gagggctccc 1560
caaaagcaga agccactatg cttcctgaac agccaatgga accatgagcc aattaaacct 1620
cttcttta                                     1628

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<210> 10
<211> 348
<212> PRT
<213> Homo sapiens

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<220>
<223> human G-protein coupled receptor (GPCR) TGR60 Sequence 2

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<400> 10
Met Pro Ala Asn Phe Thr Glu Gly Ser Phe Asp Ser Ser Gly Thr Gly
 1          5          10          15
Gln Thr Leu Asp Ser Ser Pro Val Ala Cys Thr Glu Thr Val Thr Phe
          20          25          30
Thr Glu Val Val Glu Gly Lys Glu Trp Gly Ser Phe Tyr Tyr Ser Phe
          35          40          45
Lys Thr Glu Gln Leu Ile Thr Leu Trp Val Leu Phe Val Phe Thr Ile
          50          55          60
Val Gly Asn Ser Val Val Leu Phe Ser Thr Trp Arg Arg Lys Lys Lys
          65          70          75          80
Ser Arg Met Thr Phe Phe Val Thr Gln Leu Ala Ile Thr Asp Ser Phe
          85          90          95
Thr Gly Leu Val Asn Ile Leu Thr Asp Ile Asn Trp Arg Phe Thr Gly
          100          105          110
Asp Phe Thr Gly Pro Asp Leu Val Cys Arg Val Val Arg Tyr Leu Gln
          115          120          125
Val Val Leu Leu Tyr Ala Ser Thr Tyr Val Leu Val Ser Leu Ser Ile
          130          135          140
Asp Arg Tyr His Ala Ile Val Tyr Pro Met Lys Phe Leu Gln Gly Glu
          145          150          155          160
Lys Gln Ala Arg Val Leu Ile Val Ile Ala Trp Ser Leu Ser Phe Leu
          165          170          175
Phe Ser Ile Pro Thr Leu Ile Ile Phe Gly Lys Arg Thr Leu Ser Asn
          180          185          190
Gly Glu Val Gln Cys Trp Ala Leu Trp Pro Asp Asp Ser Tyr Trp Thr
          195          200          205
Pro Tyr Met Thr Ile Val Ala Phe Leu Val Tyr Phe Ile Pro Leu Thr
          210          215          220
Ile Ile Ser Ile Met Tyr Gly Ile Val Ile Arg Thr Ile Trp Ile Lys
          225          230          235          240
Ser Lys Thr Tyr Glu Thr Val Ile Ser Asn Cys Ser Asp Gly Lys Leu
          245          250          255
Cys Ser Ser Tyr Asn Arg Gly Leu Ile Ser Lys Ala Lys Ile Lys Ala
          260          265          270

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Ile	Lys	Tyr	Ser	Ile	Ile	Ile	Ile	Leu	Ala	Phe	Ile	Cys	Cys	Trp	Ser
		275					280					285			
Pro	Tyr	Phe	Leu	Phe	Asp	Ile	Leu	Asp	Asn	Phe	Asn	Leu	Leu	Pro	Asp
	290				295				300						
Thr	Gln	Glu	Arg	Phe	Tyr	Ala	Ser	Val	Ile	Ile	Gln	Asn	Leu	Pro	Ala
305					310				315						320
Leu	Asn	Ser	Ala	Ile	Asn	Pro	Leu	Ile	Tyr	Cys	Val	Phe	Ser	Ser	Ser
			325						330					335	
Ile	Ser	Phe	Pro	Cys	Arg	Ile	Ile	Asp	Gly	Asn	Asp				
			340					345							

<210> 11
 <211> 1155
 <212> DNA
 <213> Drosophila melanogaster

<220>
 <221> CDS
 <222> (1)..(1155)
 <223> Drosophila novel CG6111 sequence, pigment-dispensing factor (PDF) receptor

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 aacaagaatc gcaagtcgcg gatgaactac ttcattaaac agctggcatt ggcagatctg 180
 tgctgtgggac tgctcaacgt cctcaccgac atcatatggc gcatcacgat ttcgtggcgg 240
 gcaggcaacc tggcctgcaa ggccatccgc ttctcgcagg tctgcgtcac atactcgtcc 300
 acctacgtgc tgggtggccat gagcatcgac agatacgaag ccatacacaca ccccatgaac 360
 ttctcaaagt cgtggaaaag agcccgtcac ctgggtggctg gcgcatgggt catctcggcg 420
 ttgttttgcg tttccatcct ggttttgtac gaggagaagc tcatccaagg acatccgcaa 480
 tgctggattg agttgggttc accgatcgcc tggcagggtat acatgagcct ggtgtcggcc 540
 actctatttg ccattcctgc gctgatcata tctgcctgct atgcgatcat cgtaaagacg 600
 atttgggcaa aggggttccat ttttgtaccc acggaacgtg ctgggttttg agctgcacct 660
 gccaggaggg ccagctcgag gggcattatt ccacgggcaa aggtcaaaac ggtcaagatg 720
 acattgacca tcgtgtttgt gttcatcatc tgctggtcgc cgtatatcat cttegatctg 780
 ctgcaggctc ttggccagat tccacactca cagaccaaca ttgccatcgc caccttcac 840
 caaagtcttg caccgctgaa ctgcggcgcg aatccactaa tctattgcct cttctcatcg 900
 caggctcttc gcacatttaag tcgctttccg ccttttaagt gggtcacatg ctgctgcaag 960
 tcataaccgca acaactcgca gcaaaaccgc tgccacacgg ttggtcgctg gcttcacaac 1020
 agttgcgatt cgatgaggac actgaccact tcggtgacgg tttcccgaag gtccaccaac 1080
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 atgtcggagg tatga 1155

<210> 12
 <211> 384
 <212> PRT
 <213> Drosophila melanogaster

<220>
 <223> Drosophila novel CG6111 sequence, pigment-dispensing factor (PDF) receptor

<400> 12
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 Phe Ala Val Leu Trp Ile Leu Phe Thr Val Ile Val Leu Gly Asn Ser
 20 25 30

Ala	Val	Leu	Phe	Val	Met	Phe	Ile	Asn	Lys	Asn	Arg	Lys	Ser	Arg	Met
		35					40					45			
Asn	Tyr	Phe	Ile	Lys	Gln	Leu	Ala	Leu	Ala	Asp	Leu	Cys	Val	Gly	Leu
	50					55					60				
Leu	Asn	Val	Leu	Thr	Asp	Ile	Ile	Trp	Arg	Ile	Thr	Ile	Ser	Trp	Arg
	65				70					75					80
Ala	Gly	Asn	Leu	Ala	Cys	Lys	Ala	Ile	Arg	Phe	Ser	Gln	Val	Cys	Val
				85					90					95	
Thr	Tyr	Ser	Ser	Thr	Tyr	Val	Leu	Val	Ala	Met	Ser	Ile	Asp	Arg	Tyr
			100					105					110		
Asp	Ala	Ile	Thr	His	Pro	Met	Asn	Phe	Ser	Lys	Ser	Trp	Lys	Arg	Ala
		115					120					125			
Arg	His	Leu	Val	Ala	Gly	Ala	Trp	Leu	Ile	Ser	Ala	Leu	Phe	Ser	Leu
		130				135					140				
Pro	Ile	Leu	Val	Leu	Tyr	Glu	Glu	Lys	Leu	Ile	Gln	Gly	His	Pro	Gln
	145				150					155					160
Cys	Trp	Ile	Glu	Leu	Gly	Ser	Pro	Ile	Ala	Trp	Gln	Val	Tyr	Met	Ser
			165						170					175	
Leu	Val	Ser	Ala	Thr	Leu	Phe	Ala	Ile	Pro	Ala	Leu	Ile	Ile	Ser	Ala
			180					185					190		
Cys	Tyr	Ala	Ile	Ile	Val	Lys	Thr	Ile	Trp	Ala	Lys	Gly	Ser	Ile	Phe
		195					200					205			
Val	Pro	Thr	Glu	Arg	Ala	Gly	Phe	Gly	Ala	Ala	Pro	Ala	Arg	Arg	Ala
	210					215					220				
Ser	Ser	Arg	Gly	Ile	Ile	Pro	Arg	Ala	Lys	Val	Lys	Thr	Val	Lys	Met
	225				230					235					240
Thr	Leu	Thr	Ile	Val	Phe	Val	Phe	Ile	Ile	Cys	Trp	Ser	Pro	Tyr	Ile
			245					250						255	
Ile	Phe	Asp	Leu	Leu	Gln	Val	Phe	Gly	Gln	Ile	Pro	His	Ser	Gln	Thr
		260						265					270		
Asn	Ile	Ala	Ile	Ala	Thr	Phe	Ile	Gln	Ser	Leu	Ala	Pro	Leu	Asn	Ser
		275					280					285			
Ala	Ala	Asn	Pro	Leu	Ile	Tyr	Cys	Leu	Phe	Ser	Ser	Gln	Val	Phe	Arg
	290					295					300				
Thr	Leu	Ser	Arg	Phe	Pro	Pro	Phe	Lys	Trp	Phe	Thr	Cys	Cys	Cys	Lys
	305				310					315					320
Ser	Tyr	Arg	Asn	Asn	Ser	Gln	Gln	Asn	Arg	Cys	His	Thr	Val	Gly	Arg
			325						330					335	
Arg	Leu	His	Asn	Ser	Cys	Asp	Ser	Met	Arg	Thr	Leu	Thr	Thr	Ser	Leu
			340					345					350		
Thr	Val	Ser	Arg	Arg	Ser	Thr	Asn	Lys	Thr	Asn	Ala	Arg	Val	Val	Ile
		355				360					365				
Cys	Glu	Arg	Pro	Thr	Lys	Val	Val	Thr	Val	Pro	Ala	Met	Ser	Glu	Val
	370					375					380				

<210> 13

<211> 1191

<212> DNA

<213> *Drosophila melanogaster*

<220>

<221> CDS

<222> (1)..(1191)

<223> *Drosophila* CG6111 Celera fly genome project sequence,
pigment-dispersing factor (PDF) receptor

<400> 13

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aacaagaatc gcaagtcgcg gatgaactac ttcattaaac agctggcatt ggcagatctg 180
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tgcgtggggac tgc tcaacgt cctcaccgac atcatatggc gcatcacgat ttcgtggcgg 240
gcaggcaacc tggcctgcaa ggccatccgc ttctcgcagg tctgcgtcac atactcgtcc 300
acctacgtgc tgggtggccat gagcatcgac agatacgatg ccatcacaca ccccatgaac 360
ttctcaaagt cgtggaaaaag agcccgtcac ctgggtggctg gcgcatggct catctcggcg 420
ttgttttcgc ttcccatcct ggttttgtac gaggagaagc tcatccaagg acatccgcaa 480
tgc tggattg agttgggttc accgatcgcc tggcaggtgt acatgagcct ggtgtcggcc 540
actctatttg ccattcctgc gctgatcata tctgcctgct atgcgatcat cgtaaagacg 600
atttgggcaa aggggttccat tttgtaccc acggaacgtg ctgggttttg agctgcacct 660
gccaggaggg ccagctcgag gggcattatt ccacgggcaa aggtcaaaac ggtcaagatg 720
acattgacca tcgtgtttgt gttcatcatc tgctggtcgc cgtatatcat cttcgatctg 780
ctgcaggtct ttggccagat tccacactca cagaccaaca ttgccatcgc caccttcac 840
caaagtcttg caccgctgaa ctcggcggcg aatccactaa tctattgcct cttctcatcg 900
caggtctttc gcacattaag tcgctttccg ccttttaagt gggtcacatg ctgctgcaag 960
tcataccgca acaactcgca gcaaaaccgc tgccacacgg ttggtcgctg gcttcacaac 1020
agttgcgatt cgatgaggac actgaccact tcgttgacgg tttcccgaag gtccaccaac 1080
aagacgaacg cccgtgtggt aatctgcgaa cgtcccacca aggtgggttac cgtgccagcc 1140
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<210> 14

<211> 396

<212> PRT

<213> *Drosophila melanogaster*

<220>

<223> *Drosophila* CG6111 Celera fly genome project sequence,
pigment-dispensing factor (PDF) receptor

<400> 14

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 1          5          10          15
Phe Ala Val Leu Trp Ile Leu Phe Thr Val Ile Val Leu Gly Asn Ser
 20          25          30
Ala Val Leu Phe Val Met Phe Ile Asn Lys Asn Arg Lys Ser Arg Met
 35          40          45
Asn Tyr Phe Ile Lys Gln Leu Ala Leu Ala Asp Leu Cys Val Gly Leu
 50          55          60
Leu Asn Val Leu Thr Asp Ile Ile Trp Arg Ile Thr Ile Ser Trp Arg
 65          70          75          80
Ala Gly Asn Leu Ala Cys Lys Ala Ile Arg Phe Ser Gln Val Cys Val
 85          90          95
Thr Tyr Ser Ser Thr Tyr Val Leu Val Ala Met Ser Ile Asp Arg Tyr
100          105          110
Asp Ala Ile Thr His Pro Met Asn Phe Ser Lys Ser Trp Lys Arg Ala
115          120          125
Arg His Leu Val Ala Gly Ala Trp Leu Ile Ser Ala Leu Phe Ser Leu
130          135          140
Pro Ile Leu Val Leu Tyr Glu Glu Lys Leu Ile Gln Gly His Pro Gln
145          150          155          160
Cys Trp Ile Glu Leu Gly Ser Pro Ile Ala Trp Gln Val Tyr Met Ser
165          170          175
Leu Val Ser Ala Thr Leu Phe Ala Ile Pro Ala Leu Ile Ile Ser Ala
180          185          190
Cys Tyr Ala Ile Ile Val Lys Thr Ile Trp Ala Lys Gly Ser Ile Phe
195          200          205
Val Pro Thr Glu Arg Ala Gly Phe Gly Ala Ala Pro Ala Arg Arg Ala
210          215          220
Ser Ser Arg Gly Ile Ile Pro Arg Ala Lys Val Lys Thr Val Lys Met
225          230          235          240
Thr Leu Thr Ile Val Phe Val Phe Ile Ile Cys Trp Ser Pro Tyr Ile
245          250          255

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Ile	Phe	Asp	Leu	Leu	Gln	Val	Phe	Gly	Gln	Ile	Pro	His	Ser	Gln	Thr
			260					265					270		
Asn	Ile	Ala	Ile	Ala	Thr	Phe	Ile	Gln	Ser	Leu	Ala	Pro	Leu	Asn	Ser
		275					280					285			
Ala	Ala	Asn	Pro	Leu	Ile	Tyr	Cys	Leu	Phe	Ser	Ser	Gln	Val	Phe	Arg
		290				295				300					
Thr	Leu	Ser	Arg	Phe	Pro	Pro	Phe	Lys	Trp	Phe	Thr	Cys	Cys	Cys	Lys
305					310					315					320
Ser	Tyr	Arg	Asn	Asn	Ser	Gln	Gln	Asn	Arg	Cys	His	Thr	Val	Gly	Arg
			325					330						335	
Arg	Leu	His	Asn	Ser	Cys	Asp	Ser	Met	Arg	Thr	Leu	Thr	Thr	Ser	Leu
			340					345					350		
Thr	Val	Ser	Arg	Arg	Ser	Thr	Asn	Lys	Thr	Asn	Ala	Arg	Val	Val	Ile
		355					360					365			
Cys	Glu	Arg	Pro	Thr	Lys	Val	Val	Thr	Val	Pro	Ala	Met	Ser	Glu	Arg
	370					375					380				
Arg	Gly	Val	Ser	Leu	Lys	Gly	Asn	Thr	Asp	Ile	Leu				
385					390					395					

<210> 15
 <211> 1737
 <212> DNA
 <213> Mus sp.

<220>
 <221> CDS
 <222> (1)..(1302)
 <223> mouse G-protein coupled receptor (GPCR) TGR346a

<400> 15
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 actcgggaac agttcattca tcgctatggg ctgcgaccgc tgggtctacac tccggagctg 120
 cccgcgcgcg ctaaactggc ctttgcgctg gctggagcac tcatttttgc cctggcgctc 180
 tttggcaact ctctgggtcat ctatgtgggtg acccgcagca aggccatgcg caccgtcacc 240
 aacatcttca tctgctctct ggcaactcagt gatctgctca ttgccttctt ctgcatcccc 300
 gtcacgatgc tccagaacat ctccgacaag tggtctgggtg gtgccttcat ctgcaagatg 360
 gtgccttctg tccagtccac tgctgttggtg acggaaatcc tcaccatgac ttgcatcgct 420
 gttgagaggc accaaggact catccatcct tttaaaatga agtggcagta cactaccgca 480
 agggctttca caatcttggg tgtggtctgg ttggcagcca tcatcgtagg atcaccatg 540
 tggcacgtac aacgcctcga gattaagtat gacttcctct atgagaaaga acatgtctgc 600
 tgtttggaag agtgggccag ccccatgcac cagagaatct acaccacctt catcctcgct 660
 atcctcttcc tctgcccgtg tgtggtgatg cttgtcctct acagcaagat tggctatgaa 720
 ctgtggatca agaagagagt tggagacagt tcagcacttc agactatcca cgggaaagaa 780
 atgtccaaaa tagccaggaa gaagaagcgg gctgtcggtt tgatgggtgac agtgggtggc 840
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 tttgaaaaag agtatgatga tgtcacaatc aagatgggtt ttgctgttgc acaaacaatt 960
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 aagaattttt tgtctgcggg ttgttattgc atagtaagag aaaccttctc ccaggacag 1080
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 ctgaacatca taatgtagtt tgtagtgtgc tgtaaacgtt tgtaaaatca gcctttggaa 1680
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<210> 16
 <211> 433
 <212> PRT
 <213> Mus sp.

<220>

<223> mouse G-protein coupled receptor (GPCR) TGR346a

<400> 16

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Ala	His	Asn	Leu	Thr	Arg	Glu	Gln	Phe	Ile	His	Arg	Tyr	Gly	Leu	Arg
		20					25						30		
Pro	Leu	Val	Tyr	Thr	Pro	Glu	Leu	Pro	Ala	Arg	Ala	Lys	Leu	Ala	Phe
		35					40					45			
Ala	Leu	Ala	Gly	Ala	Leu	Ile	Phe	Ala	Leu	Ala	Leu	Phe	Gly	Asn	Ser
		50				55					60				
Leu	Val	Ile	Tyr	Val	Val	Thr	Arg	Ser	Lys	Ala	Met	Arg	Thr	Val	Thr
		65			70					75				80	
Asn	Ile	Phe	Ile	Cys	Ser	Leu	Ala	Leu	Ser	Asp	Leu	Leu	Ile	Ala	Phe
				85					90					95	
Phe	Cys	Ile	Pro	Val	Thr	Met	Leu	Gln	Asn	Ile	Ser	Asp	Lys	Trp	Leu
			100					105					110		
Gly	Gly	Ala	Phe	Ile	Cys	Lys	Met	Val	Pro	Phe	Val	Gln	Ser	Thr	Ala
		115					120					125			
Val	Val	Thr	Glu	Ile	Leu	Thr	Met	Thr	Cys	Ile	Ala	Val	Glu	Arg	His
		130				135					140				
Gln	Gly	Leu	Ile	His	Pro	Phe	Lys	Met	Lys	Trp	Gln	Tyr	Thr	Thr	Arg
		145			150					155					160
Arg	Ala	Phe	Thr	Ile	Leu	Gly	Val	Val	Trp	Leu	Ala	Ala	Ile	Ile	Val
				165					170					175	
Gly	Ser	Pro	Met	Trp	His	Val	Gln	Arg	Leu	Glu	Ile	Lys	Tyr	Asp	Phe
			180					185					190		
Leu	Tyr	Glu	Lys	Glu	His	Val	Cys	Cys	Leu	Glu	Glu	Trp	Ala	Ser	Pro
		195					200					205			
Met	His	Gln	Arg	Ile	Tyr	Thr	Thr	Phe	Ile	Leu	Val	Ile	Leu	Phe	Leu
		210				215					220				
Leu	Pro	Leu	Val	Val	Met	Leu	Val	Leu	Tyr	Ser	Lys	Ile	Gly	Tyr	Glu
		225			230					235					240
Leu	Trp	Ile	Lys	Lys	Arg	Val	Gly	Asp	Ser	Ser	Ala	Leu	Gln	Thr	Ile
				245				250						255	
His	Gly	Lys	Glu	Met	Ser	Lys	Ile	Ala	Arg	Lys	Lys	Lys	Arg	Ala	Val
			260					265					270		
Val	Met	Met	Val	Thr	Val	Val	Ala	Leu	Phe	Ala	Ala	Cys	Trp	Ala	Pro
		275					280					285			
Phe	His	Val	Val	His	Met	Met	Val	Glu	Tyr	Ser	Asn	Phe	Glu	Lys	Glu
		290				295					300				
Tyr	Asp	Asp	Val	Thr	Ile	Lys	Met	Val	Phe	Ala	Val	Ala	Gln	Thr	Ile
					310					315					320
Gly	Phe	Phe	Asn	Ser	Ile	Cys	Asn	Pro	Phe	Val	Tyr	Ala	Phe	Met	Asn
			325						330					335	
Glu	Asn	Phe	Lys	Lys	Asn	Phe	Leu	Ser	Ala	Val	Cys	Tyr	Cys	Ile	Val
			340					345					350		
Arg	Glu	Thr	Phe	Ser	Pro	Gly	Gln	Lys	Pro	Gly	Asn	Ser	Gly	Ile	Ser
		355					360					365			
Met	Met	Gln	Lys	Arg	Ala	Lys	Leu	Ser	Arg	Ser	Gln	Arg	Pro	Val	Ala
		370				375					380				
Glu	Ala	Lys	Gly	Asp	Leu	Phe	Ser	Asp	Ala	Asn	Val	Asp	Val	Lys	Leu
					390					395					400
Cys	Glu	Gln	Pro	Gly	Glu	Lys	Arg	Gln	Leu	Lys	Arg	Gln	Leu	Ala	Phe
				405					410					415	

Phe Ser Ser Glu Leu Ser Glu Asn Ser Thr Phe Gly Ser Gly His Glu
 420 425 430
 Leu

<210> 17
 <211> 1772
 <212> DNA
 <213> Mus sp.

<220>
 <221> CDS
 <222> (1)..(1251)
 <223> mouse G-protein coupled receptor (GPCR) TGR346b

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 gcgcgcgcca ggctggccct cctgctgggtc ggcagctcga tctttgccct ggcgctcttc 180
 ggcaacgccc tggtagtcta tgtggtgacc cgcagcaagg ccacgacgac cgtcaccaac 240
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 ccatttgtcc agtgcactgc cattgtgaca gaaatcctta ctatgacctg cattgctgtg 420
 gaaaggcacc agggacttgt ccacccctttt aaaatgaagc ggcagtacac caatcaaaga 480
 gctttcacia tgctagggtg ggtgtggctg gtggccatca tcataggatc acccatgtgg 540
 catgtgcagc gacttgagat taagtatgac ttcctatatg aaaaagaaca catctgctgc 600
 ctggaagagt ggagcagccc cgtgcaccag aagatctaca ccaccttcac ccttgtcacc 660
 ctcttctctg taccactgtt gctgctctct gtcctctacg ggaaaatcgg ttatgagctt 720
 tggatcaaga aaagaatcgg ggatggctca gtgctccgaa ctattcatgg aaaagaaatg 780
 ttcaaaatag ccagaaagaa gaagcgagct gtgacatga tggtagacag cgtggttctc 840
 tttgtgtgt gctgggcacc tttccacatc gttcacatga tgattgaata cagtaatttt 900
 gaaaaggaat atgatgaagt cacaatcaag atgatttttg ctatagtga aataattgga 960
 tttttcaact ccactgttaa tcccattatt tatgcaacta tgaatgaaaa cttcaaaaaa 1020
 aactttgtgt ctgccgtttg ctattgcatt gtgaaggaaa caccttcttc agcacggaag 1080
 catggaagtt caggagctat ggtgatgcac aggagggcaa agttagctgc aagagagaat 1140
 cctgtagaga tcaaaggaga agcatttggg ggcagcaaca tcgatatcaa gtggtgtgaa 1200
 cagccagaaa agaagaagag gagatcaaaa gtggcatctt gtccctctta gttccgaatt 1260
 tctgagagct ctgctgtaga cgtgaacact gtaccaatgt cttcagaatg agtatctgtc 1320
 atactgtaac cgaaagaaaa tgattttgag aaaaagccag agagctttca tattaataat 1380
 gttgacaaac actcagaagg caggacagg ggattcaaga gtttaaagtc atccttagct 1440
 gcacgataag tttgaggata acctgggcta caagagaccc tgtctcaaga agccataata 1500
 attaaaacaa ccacccctta ctaatgataa tgacaaagta tttttccatt gaaaatacat 1560
 gtaagctgca attttgaaaa attattgaac cacccttggtg attaatagat gaagtttaaa 1620
 aaaatttaaa tgtgttttta ttgtatgtat atggttggtt tacctgtgta tatgtctttc 1680
 agtaacttgt ataaaactca atgatctcag ctagtaactt tcttctgtgt ggtcaatgtg 1740
 atatgatttc ctatatattg ctaaattgaa tg 1772

<210> 18
 <211> 416
 <212> PRT
 <213> Mus sp.

<220>
 <221> CDS
 <222> (1)..(1302)
 <223> mouse G-protein coupled receptor (GPCR) TGR346b

<400> 18
 Met Ser Trp Asn Leu Thr Ala Glu Gln Leu Ser Ala Leu Leu Arg Leu
 1 5 10 15

His	Asn	Leu	Thr	Arg	Ala	Gln	Phe	Ile	Ala	His	Tyr	Gly	Leu	Arg	Pro
			20					25					30		
Leu	Val	Leu	Thr	Pro	Gln	Leu	Pro	Ala	Arg	Ala	Arg	Leu	Ala	Leu	Leu
		35					40					45			
Leu	Val	Gly	Met	Leu	Ile	Phe	Ala	Leu	Ala	Leu	Phe	Gly	Asn	Ala	Leu
	50					55					60				
Val	Val	Tyr	Val	Val	Thr	Arg	Ser	Lys	Ala	Met	Arg	Thr	Val	Thr	Asn
	65				70					75					80
Ile	Phe	Ile	Cys	Ser	Leu	Ala	Leu	Ser	Asp	Leu	Leu	Ile	Val	Phe	Phe
			85						90					95	
Cys	Ile	Pro	Val	Thr	Met	Leu	Gln	Asn	Val	Ser	Asp	Thr	Trp	Leu	Gly
			100					105					110		
Gly	Ala	Phe	Ile	Cys	Lys	Met	Val	Pro	Phe	Val	Gln	Cys	Thr	Ala	Ile
		115					120					125			
Val	Thr	Glu	Ile	Leu	Thr	Met	Thr	Cys	Ile	Ala	Val	Glu	Arg	His	Gln
	130					135					140				
Gly	Leu	Val	His	Pro	Phe	Lys	Met	Lys	Arg	Gln	Tyr	Thr	Asn	Gln	Arg
	145				150					155					160
Ala	Phe	Thr	Met	Leu	Gly	Val	Val	Trp	Leu	Val	Ala	Ile	Ile	Ile	Gly
				165					170					175	
Ser	Pro	Met	Trp	His	Val	Gln	Arg	Leu	Glu	Ile	Lys	Tyr	Asp	Phe	Leu
			180					185					190		
Tyr	Glu	Lys	Glu	His	Ile	Cys	Cys	Leu	Glu	Glu	Trp	Ser	Ser	Pro	Val
		195				200						205			
His	Gln	Lys	Ile	Tyr	Thr	Thr	Phe	Ile	Leu	Val	Thr	Leu	Phe	Leu	Leu
	210					215					220				
Pro	Leu	Leu	Leu	Leu	Ser	Val	Leu	Tyr	Gly	Lys	Ile	Gly	Tyr	Glu	Leu
	225				230					235					240
Trp	Ile	Lys	Lys	Arg	Ile	Gly	Asp	Gly	Ser	Val	Leu	Arg	Thr	Ile	His
				245					250					255	
Gly	Lys	Glu	Met	Phe	Lys	Ile	Ala	Arg	Lys	Lys	Lys	Arg	Ala	Val	Ile
			260					265					270		
Met	Met	Val	Thr	Val	Val	Val	Leu	Phe	Ala	Val	Cys	Trp	Ala	Pro	Phe
		275					280					285			
His	Ile	Val	His	Met	Met	Ile	Glu	Tyr	Ser	Asn	Phe	Glu	Lys	Glu	Tyr
	290					295					300				
Asp	Glu	Val	Thr	Ile	Lys	Met	Ile	Phe	Ala	Ile	Val	Gln	Ile	Ile	Gly
	305				310					315					320
Phe	Phe	Asn	Ser	Ile	Cys	Asn	Pro	Ile	Ile	Tyr	Ala	Leu	Met	Asn	Glu
				325					330					335	
Asn	Phe	Lys	Lys	Asn	Phe	Val	Ser	Ala	Val	Cys	Tyr	Cys	Ile	Val	Lys
			340					345					350		
Glu	Thr	Pro	Ser	Ser	Ala	Arg	Lys	His	Gly	Ser	Ser	Gly	Ala	Met	Val
		355					360					365			
Met	His	Arg	Arg	Ala	Lys	Leu	Ala	Ala	Arg	Glu	Asn	Pro	Val	Glu	Ile
	370					375					380				
Lys	Gly	Glu	Ala	Phe	Gly	Gly	Ser	Asn	Ile	Asp	Ile	Lys	Trp	Cys	Glu
	385				390					395					400
Gln	Pro	Glu	Lys	Lys	Lys	Arg	Arg	Ser	Lys	Val	Ala	Ser	Cys	Pro	Leu
				405					410					415	

<210> 19

<211> 402

<212> PRT

<213> Homo sapiens

<220>

<223> human melanin-concentrating hormone receptor
(MCHr1)

<400> 19

Met	Leu	Cys	Pro	Ser	Lys	Thr	Asp	Gly	Ser	Gly	His	Ser	Gly	Arg	Ile
1				5					10					15	
His	Gln	Glu	Thr	His	Gly	Glu	Gly	Lys	Arg	Asp	Lys	Ile	Ser	Asn	Ser
			20					25					30		
Glu	Gly	Arg	Glu	Asn	Gly	Gly	Arg	Gly	Phe	Gln	Met	Asn	Gly	Gly	Ser
		35					40					45			
Leu	Glu	Ala	Glu	His	Ala	Ser	Arg	Met	Ser	Val	Leu	Arg	Ala	Lys	Pro
		50				55					60				
Met	Ser	Asn	Ser	Gln	Arg	Leu	Leu	Leu	Leu	Ser	Pro	Gly	Ser	Pro	Pro
65				70						75				80	
Arg	Thr	Gly	Ser	Ile	Ser	Tyr	Ile	Asn	Ile	Ile	Met	Pro	Ser	Val	Phe
				85				90						95	
Gly	Thr	Ile	Cys	Leu	Leu	Gly	Ile	Ile	Gly	Asn	Ser	Thr	Val	Ile	Phe
			100				105						110		
Ala	Val	Val	Lys	Lys	Ser	Lys	Leu	His	Trp	Cys	Asn	Asn	Val	Pro	Asp
		115					120					125			
Ile	Phe	Ile	Ile	Asn	Leu	Ser	Val	Val	Asp	Leu	Leu	Phe	Leu	Leu	Gly
130					135					140					
Met	Pro	Phe	Met	Ile	His	Gln	Leu	Met	Gly	Asn	Gly	Val	Trp	His	Phe
145				150						155				160	
Gly	Glu	Thr	Met	Cys	Thr	Leu	Ile	Thr	Ala	Met	Asp	Ala	Asn	Ser	Gln
				165				170						175	
Phe	Thr	Ser	Thr	Tyr	Ile	Leu	Thr	Ala	Met	Ala	Ile	Asp	Arg	Tyr	Leu
			180				185						190		
Ala	Thr	Val	His	Pro	Ile	Ser	Ser	Thr	Lys	Phe	Arg	Lys	Pro	Ser	Val
		195					200					205			
Ala	Thr	Leu	Val	Ile	Cys	Leu	Leu	Trp	Ala	Leu	Ser	Phe	Ile	Ser	Ile
210					215					220					
Thr	Pro	Val	Trp	Leu	Tyr	Ala	Arg	Leu	Ile	Pro	Phe	Pro	Gly	Gly	Ala
225				230						235				240	
Val	Gly	Cys	Gly	Ile	Arg	Leu	Pro	Asn	Pro	Asp	Thr	Asp	Leu	Tyr	Trp
				245				250						255	
Phe	Thr	Leu	Tyr	Gln	Phe	Phe	Leu	Ala	Phe	Ala	Leu	Pro	Phe	Val	Val
			260				265						270		
Ile	Thr	Ala	Ala	Tyr	Val	Arg	Ile	Leu	Gln	Arg	Met	Thr	Ser	Ser	Val
		275				280						285			
Ala	Pro	Ala	Ser	Gln	Arg	Ser	Ile	Arg	Leu	Arg	Thr	Lys	Arg	Val	Thr
290				295							300				
Arg	Thr	Ala	Ile	Ala	Ile	Cys	Leu	Val	Phe	Phe	Val	Cys	Trp	Ala	Pro
305				310					315					320	
Tyr	Tyr	Val	Leu	Gln	Leu	Thr	Gln	Leu	Ser	Ile	Ser	Arg	Pro	Thr	Leu
			325				330						335		
Thr	Phe	Val	Tyr	Leu	Tyr	Asn	Ala	Ala	Ile	Ser	Leu	Gly	Tyr	Ala	Asn
			340			345						350			
Ser	Cys	Leu	Asn	Pro	Phe	Val	Tyr	Ile	Val	Leu	Cys	Glu	Thr	Phe	Arg
		355			360						365				
Lys	Arg	Leu	Val	Leu	Ser	Val	Lys	Pro	Ala	Ala	Gln	Gly	Gln	Leu	Arg
370					375					380					
Ala	Val	Ser	Asn	Ala	Gln	Thr	Ala	Asp	Glu	Glu	Arg	Thr	Glu	Ser	Lys
385				390					395						400

Gly Thr

<210> 20

<211> 391

<212> PRT

<213> Homo sapiens

<220>

<223> human somatostatin receptor 1 (SSTR1)

<400> 20

Met	Phe	Pro	Asn	Gly	Thr	Ala	Ser	Ser	Pro	Ser	Ser	Ser	Pro	Ser	Pro
1				5					10					15	
Ser	Pro	Gly	Ser	Cys	Gly	Glu	Gly	Gly	Gly	Ser	Arg	Gly	Pro	Gly	Ala
			20					25					30		
Gly	Ala	Ala	Asp	Gly	Met	Glu	Glu	Pro	Gly	Arg	Asn	Ala	Ser	Gln	Asn
		35					40					45			
Gly	Thr	Leu	Ser	Glu	Gly	Gln	Gly	Ser	Ala	Ile	Leu	Ile	Ser	Phe	Ile
	50					55					60				
Tyr	Ser	Val	Val	Cys	Leu	Val	Gly	Leu	Cys	Gly	Asn	Ser	Met	Val	Ile
65					70					75					80
Tyr	Val	Ile	Leu	Arg	Tyr	Ala	Lys	Met	Lys	Thr	Ala	Thr	Asn	Ile	Tyr
				85					90					95	
Ile	Leu	Asn	Leu	Ala	Ile	Ala	Asp	Glu	Leu	Leu	Met	Leu	Ser	Val	Pro
			100					105					110		
Phe	Leu	Val	Thr	Ser	Thr	Leu	Leu	Arg	His	Trp	Pro	Phe	Gly	Ala	Leu
		115					120					125			
Leu	Cys	Arg	Leu	Val	Leu	Ser	Val	Asp	Ala	Val	Asn	Met	Phe	Thr	Ser
	130					135					140				
Ile	Tyr	Cys	Leu	Thr	Val	Leu	Ser	Val	Asp	Arg	Tyr	Val	Ala	Val	Val
145					150					155					160
His	Pro	Ile	Lys	Ala	Ala	Arg	Tyr	Arg	Arg	Pro	Thr	Val	Ala	Lys	Val
			165					170						175	
Val	Asn	Leu	Gly	Val	Trp	Val	Leu	Ser	Leu	Leu	Val	Ile	Leu	Pro	Ile
		180					185					190			
Val	Val	Phe	Ser	Arg	Thr	Ala	Ala	Asn	Ser	Asp	Gly	Thr	Val	Ala	Cys
		195					200					205			
Asn	Met	Leu	Met	Pro	Glu	Pro	Ala	Gln	Arg	Trp	Leu	Val	Gly	Phe	Val
	210					215					220				
Leu	Tyr	Thr	Phe	Leu	Met	Gly	Phe	Leu	Leu	Pro	Val	Gly	Ala	Ile	Cys
225					230					235					240
Leu	Cys	Tyr	Val	Leu	Ile	Ile	Ala	Lys	Met	Arg	Met	Val	Ala	Leu	Lys
			245					250						255	
Ala	Gly	Trp	Gln	Gln	Arg	Lys	Arg	Ser	Glu	Arg	Lys	Ile	Thr	Leu	Met
			260				265						270		
Val	Met	Met	Val	Val	Met	Val	Phe	Val	Ile	Cys	Trp	Met	Pro	Phe	Tyr
		275					280					285			
Val	Val	Gln	Leu	Val	Asn	Val	Phe	Ala	Glu	Gln	Asp	Asp	Ala	Thr	Val
	290				295						300				
Ser	Gln	Leu	Ser	Val	Ile	Leu	Gly	Tyr	Ala	Asn	Ser	Cys	Ala	Asn	Pro
305					310					315					320
Ile	Leu	Tyr	Gly	Phe	Leu	Ser	Asp	Asn	Phe	Lys	Arg	Ser	Phe	Gln	Arg
			325					330						335	
Ile	Leu	Cys	Leu	Ser	Trp	Met	Asp	Asn	Ala	Ala	Glu	Glu	Pro	Val	Asp
		340					345						350		
Tyr	Tyr	Ala	Thr	Ala	Leu	Lys	Ser	Arg	Ala	Tyr	Ser	Val	Glu	Asp	Phe
		355				360						365			
Gln	Pro	Glu	Asn	Leu	Glu	Ser	Gly	Gly	Val	Phe	Arg	Asn	Gly	Thr	Cys
	370				375						380				
Thr	Ser	Arg	Ile	Thr	Thr	Leu									
385					390										

<210> 21

<211> 200

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:flexible linker

<220>
 <221> MOD_RES
 <222> (6)..(200)
 <223> Gly at positions 6-200 may be present or absent

<400> 21
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 1 5 10 15
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 20 25 30
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 35 40 45
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 50 55 60
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 65 70 75 80
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 85 90 95
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 100 105 110
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 115 120 125
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 130 135 140
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 145 150 155 160
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 165 170 175
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 180 185 190
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 195 200

<210> 22
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:TGR342Left PCR
 expression profiling primer

<400> 22
 ggaaagtcca cgaacaatga a

21

<210> 23
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:TGR342Right PCR
 expression profiling primer

<400> 23
 tgaataagaa aaggcattcc aac

23

<210> 24
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:Left primer

 <400> 24
 ccagtgtggt agatacagtc atcctccctt c 31

 <210> 25
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:Right primer

 <400> 25
 actcactata gggctcgagc ggc 23

 <210> 26
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:TGR60L: Fwd PCR
 primer

 <400> 26
 caccatgccca gccaaacttca cagagggcag c 31

 <210> 27
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:TGR60L: Rev PCR
 primer

 <400> 27
 ctagatgaat tctggcttgg acag 24

 <210> 28
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:TGR60S: Fwd PCR
 primer

 <400> 28
 caccatgccca gccaaacttca cagagggcag c 31

<210> 29
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:TGR60S: Rev PCR
 primer

 <400> 29
 ctagtcattt ccatctatga tcctgca 27

 <210> 30
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:TGR60: Forward
 primer

 <400> 30
 ctggagcctg tcttttctgt tctcc 25

 <210> 31
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:TGR60: Reverse
 primer

 <400> 31
 ggcaggttct gaatgatcac agagg 25

 <210> 32
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:CG6111 PCR
 Forward primer

 <400> 32
 atgaaatgtg accacacttt gtcc 24

 <210> 33
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:CG6111 PCR
 Reverse primer

<400> 33
tgccttcaca ggatgtccgt gttc

24

<210> 34
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:CG611 Celera
fly genome project protein carboxy terminus

<400> 34
Arg Arg Gly Val Ser Leu Lys Gly Asn Thr Asp Ile Leu
1 5 10

<210> 35
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:TGR339Left PCR
primer

<400> 35
atcccccttca atgtgtcctc

20

<210> 36
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:TGR339Right PCR
primer

<400> 36
gcagtagccc caggtagtgt

20

<210> 37
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:TGR346Left PCR
expression profiling primer

<400> 37
gcttttcacaa tgctaggtga gg

22

<210> 38
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:TGR346Right PCR
 expression profiling primer

 <400> 38
 agcaagatgt cgtttgagct tt 22

 <210> 39
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:ms346a Fwd
 primer for FLcloning

 <400> 39
 caccatgcag gcgctcaaca tcaccgc 27

 <210> 40
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:ms346a Rev
 primer for FLcloning

 <400> 40
 ttacagttca tgtccactgc cgaaagta 28

 <210> 41
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:ms346b Fwd
 primer for FLcloning

 <400> 41
 caccatgtcg tggaacttga ccgcgga 27

 <210> 42
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:ms346b Rev
 primer for FLcloning

 <400> 42
 ctaaagagga caagatgccca cttttga 27

<210> 43
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:ms346a RACE1
 primer

 <400> 43
 gctctttggc aactctctgg tcac
25

<210> 44
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:ms346a RACE2
 primer

 <400> 44
 gcacgtacaa cgcctcgaga ttaag
25

<210> 45
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:ms346a RACE3
 primer

 <400> 45
 accttcatcc tcgtcatcct cttcc
25

<210> 46
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:ms346b RACE1
 primer

 <400> 46
 acgccctggg agtctatgtg gtgac
25

<210> 47
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:ms346b RACE2
 primer

<400> 47
 tgcaccagaa gatctacacc accttc 26

<210> 48
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:ms346b RACE3
 primer

<400> 48
 attctttggca ccctcttcct gctac 25

<210> 49
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:ms346a Fwd QPCR
 primer

<400> 49
 aaggcaactc aagcgacagc 20

<210> 50
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:ms346a Rev QPCR
 primer

<400> 50
 caaatgatat tagctatgag gatatcatta ca 32

<210> 51
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:ms346a probe

<220>
 <221> modified_base
 <222> (1)
 <223> n = 6FAM-modified c

<220>
 <221> modified_base
 <222> (31)
 <223> n = TAMRA-modified a

<400> 51
 ntgaaaactc tacttttcggc agtggacatg n 31

<210> 52
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:ms346b Fwd QPCR primer

<400> 52
 tcttgctctc tttagttccg aatttc 26

<210> 53
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:ms346b Rev QPCR primer

<400> 53
 ttcgattaca gtatgacaga tactcattct 30

<210> 54
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:ms346b probe

<220>
 <221> modified_base
 <222> (1)
 <223> n = 6FAM-modified c

<220>
 <221> modified_base
 <222> (33)
 <223> n = TAMRA-modified c

<400> 54
 ntctgctgta gacgtgaaca ctgtaccaat gtn 33